

In the specification

1. Please Amend Table 2B on page 28 as follows:

Table 2B Polymerase Domain Mutations in Various DNA Polymerases

| Enzyme | Domain (bp) | Domain sequence | Predicted Mutations for Reducing DNA Polymerase Activity# |
|-----------|----------------|-----------------|-----------------------------------------------------------|
| | DXXSLYP | | |
| Pfu | 405-411 | DFRALYP | D405 (D405E) |
| Tgo | 404-410 | DFRSLYP | D404 (D404E) |
| KOD | 404-410 | DFRSLYP | D404 (D404E) |
| Vent | 407-413 | DFRSLYP | D407 [(D404E)] <u>D407E</u> |
| Deep Vent | 405-411 | DFRSLYP | D405 [(D404E)] <u>D405E</u> |
| | YXDTDS | | |
| Pfu | 539-544 | YIDTDG | T542, D543 (T542P; D543G) |
| Tgo | 538-543 | YADTDG | T541, D542 (T541P; D542G) |
| KOD | 538-543 | YSDTDG | T541, D542 (T541P; D542G) |
| Vent | 541-546 | YADTDG | T544, D545 (T544P; D545G) |
| Deep Vent | 539-544 | YIDTDG | T542, D543 (T542P; D543G) |
| | KXY | | |
| Pfu | 593-595 | KRY | K593 (K593T) |
| Tgo | 592-594 | KKY | K592 (K592T) |
| KOD | 592-594 | KKY | K592 (K592T) |
| Vent | 595-597 | KRY | K595 (K595T) |
| Deep | | | |

| | | | |
|------|---------|-----|--------------|
| Vent | 593-595 | KKY | K593 (K593T) |
|------|---------|-----|--------------|

2. On page 19, before the full paragraph starting with “Enzymes possessing 3’-5’ exonuclease activity” and ends with “Preferably, the enzyme comprising 3’-5’ exonuclease activity is a DNA polymerase,” please add the following text:

--Amino acid sequence of JDF-3 DNA polymerase (Sequence 2 of WO 01/32887):

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Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Asn Gly Lys Pro Val Ile
1           5           10           15
Arg Val Phe Lys Lys Glu Asn Gly Glu Phe Arg Ile Glu Tyr Asp Arg
           20           25           30
Glu Phe Glu Pro Tyr Phe Tyr Ala Leu Leu Arg Asp Asp Ser Ala Ile
           35           40           45
Glu Glu Ile Lys Lys Ile Thr Ala Glu Arg His Gly Arg Val Val Lys
           50           55           60
Val Lys Arg Ala Glu Lys Val Lys Lys Lys Phe Leu Gly Arg Ser Val
65           70           75           80
Glu Val Trp Val Leu Tyr Phe Thr His Pro Gln Asp Val Pro Ala Ile
           85           90           95
Arg Asp Lys Ile Arg Lys His Pro Ala Val Ile Asp Ile Tyr Glu Tyr
           100          105          110
Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
           115          120          125
Met Glu Gly Glu Glu Glu Leu Lys Leu Met Ser Phe Asp Ile Glu Thr
           130          135          140
Leu Tyr His Glu Gly Glu Glu Phe Gly Thr Gly Pro Ile Leu Met Ile
145          150          155          160

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Tyr | Ala | Asp | Glu | Ser | Glu | Ala | Arg | Val | Ile | Thr | Trp | Lys | Lys | Ile | | |
| | | | | 165 | | | | | 170 | | | | | | | 175 | |
| Asp | Leu | Pro | Tyr | Val | Glu | Val | Val | Ser | Thr | Glu | Lys | Glu | Met | Ile | Lys | | |
| | | | | 180 | | | | | 185 | | | | | | | 190 | |
| Arg | Phe | Leu | Arg | Val | Val | Lys | Glu | Lys | Asp | Pro | Asp | Val | Leu | Ile | Thr | | |
| | | | | 195 | | | | | 200 | | | | | | | 205 | |
| Tyr | Asn | Gly | Asp | Asn | Phe | Asp | Phe | Ala | Tyr | Leu | Lys | Lys | Arg | Cys | Glu | | |
| | | | | 210 | | | | | 215 | | | | | | | 220 | |
| Lys | Leu | Gly | Val | Ser | Phe | Thr | Leu | Gly | Arg | Asp | Gly | Ser | Glu | Pro | Lys | | |
| | | | | 225 | | | | | 230 | | | | | 235 | | | 240 |
| Ile | Gln | Arg | Met | Gly | Asp | Arg | Phe | Ala | Val | Glu | Val | Lys | Gly | Arg | Val | | |
| | | | | 245 | | | | | 250 | | | | | | | 255 | |
| His | Phe | Asp | Leu | Tyr | Pro | Val | Ile | Arg | Arg | Thr | Ile | Asn | Leu | Pro | Thr | | |
| | | | | 260 | | | | | 265 | | | | | | | 270 | |
| Tyr | Thr | Leu | Glu | Ala | Val | Tyr | Glu | Ala | Val | Phe | Gly | Lys | Pro | Lys | Glu | | |
| | | | | 275 | | | | | 280 | | | | | | | 285 | |
| Lys | Val | Tyr | Ala | Glu | Glu | Ile | Ala | Thr | Ala | Trp | Glu | Thr | Gly | Glu | Gly | | |
| | | | | 290 | | | | | 295 | | | | | | | 300 | |
| Leu | Glu | Arg | Val | Ala | Arg | Tyr | Ser | Met | Glu | Asp | Ala | Arg | Val | Thr | Tyr | | |
| | | | | 305 | | | | | 310 | | | | | 315 | | | 320 |
| Glu | Leu | Gly | Arg | Glu | Phe | Phe | Pro | Met | Glu | Ala | Gln | Leu | Ser | Arg | Leu | | |
| | | | | 325 | | | | | 330 | | | | | | | 335 | |
| Ile | Gly | Gln | Gly | Leu | Trp | Asp | Val | Ser | Arg | Ser | Ser | Thr | Gly | Asn | Leu | | |
| | | | | 340 | | | | | 345 | | | | | | | 350 | |
| Val | Glu | Trp | Phe | Leu | Leu | Arg | Lys | Ala | Tyr | Glu | Arg | Asn | Glu | Leu | Ala | | |
| | | | | 355 | | | | | 360 | | | | | | | 365 | |

| | |
|-----------------------------------------------------------------|-----------------------------------------------------|
| Pro Asn Lys | Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Gly Gly Tyr |
| 370 | 375 380 |
| Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Asp Asn Ile | |
| 385 | 390 395 400 |
| Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His | |
| | 405 410 415 |
| Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Ser Tyr Asp | |
| | 420 425 430 |
| Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe | |
| | 435 440 445 |
| Ile Pro Ser Leu Leu Gly Asn Leu Leu Glu Glu Arg Gln Lys Ile Lys | |
| | 450 455 460 |
| Arg Lys Met Lys Ala Thr Leu Asp Pro Leu Glu Lys Asn Leu Leu Asp | |
| 465 | 470 475 480 |
| Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly Tyr | |
| | 485 490 495 |
| Tyr Gly Tyr Ala Arg Ala Arg Trp Tyr Cys Arg Glu Cys Ala Glu Ser | |
| | 500 505 510 |
| Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Met Val Ile Arg Glu Leu | |
| | 515 520 525 |
| Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ala Asp Thr Asp Gly Leu | |
| | 530 535 540 |
| His Ala Thr Ile Pro Gly Ala Asp Ala Glu Thr Val Lys Lys Lys Ala | |
| 545 | 550 555 560 |
| Met Glu Phe Leu Asn Tyr Ile Asn Pro Lys Leu Pro Gly Leu Leu Glu | |
| | 565 570 575 |
| Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys Lys | |

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|-----------------------------------------------------------------|-----|-----|
| 580 | 585 | 590 |
| Lys Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Thr Thr Arg Gly Leu | | |
| 595 | 600 | 605 |
| Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala | | |
| 610 | 615 | 620 |
| Arg Val Leu Glu Ala Ile Leu Arg His Gly Asp Val Glu Glu Ala Val | | |
| 625 | 630 | 635 |
| Arg Ile Val Arg Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro | | |
| 645 | 650 | 655 |
| Pro Glu Lys Leu Val Ile His Glu Gln Ile Thr Arg Glu Leu Lys Asp | | |
| 660 | 665 | 670 |
| Tyr Lys Ala Thr Gly Pro His Val Ala Ile Ala Lys Arg Leu Ala Ala | | |
| 675 | 680 | 685 |
| Arg Gly Val Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu | | |
| 690 | 695 | 700 |
| Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe | | |
| 705 | 710 | 715 |
| Asp Pro Thr Lys His Lys Tyr Asp Ala Asp Tyr Tyr Ile Glu Asn Gln | | |
| 725 | 730 | 735 |
| Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys | | |
| 740 | 745 | 750 |
| Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Gly Ala Trp | | |
| 755 | 760 | 765 |
| Leu Lys Pro Lys Gly Lys Lys Lys (SEQ ID NO: 10) | | |
| 770 | 775 | |

--Nucleotide sequence of JDF-3 DNA polymerase (Sequence 1 of WO 01/32887)

| | |
|--------------------------------------------------------------------|------|
| atgacacctg acgttgatta catcaccgag aatggaaagc ccgtcatcag ggtcttcaag | 60 |
| aaggagaacg gcgagttcag gattgaatac gaccgcgagt tcgagcccta cttctacgcg | 120 |
| ctcctcaggg acgactctgc catcgaagaa atcaaaaaga taaccgcgga gaggcacggc | 180 |
| agggtcgtta aggttaagcg cgcggagaag gtgaagaaaa agttcctcgg caggctctgtg | 240 |
| gaggctctggg tcctctactt cacgcacccg caggacgttc cggcaatccg cgacaaaata | 300 |
| aggaagcacc ccgcgggtcat cgacatctac gagtacgaca tacccttcgc caagcgctac | 360 |
| ctcatagaca agggcctaata cccgatggaa ggtgaggaag agcttaaact catgtccttc | 420 |
| gacatcgaga cgctctacca cgagggagaa gagtttgga cggggccgat tctgatgata | 480 |
| agctacgccg atgaaagcga ggcgcgcgtg ataacctgga agaagatcga ccttccttac | 540 |
| gttgagggtt tctccaccga gaaggagatg attaagcgct tcttgagggt cgtaaggag | 600 |
| aaggacccgg acgtgctgat aacatacaac ggcgacaact tcgacttcgc ctacctgaaa | 660 |
| aagcgctgtg agaagcttgg cgtgagcttt accctcggga gggacgggag cgagccgaag | 720 |
| atacagcgca tgggggacag gtttgcggtc gaggtgaagg gcagggatca cttcgacctt | 780 |
| tatccagtca taaggcgac cataaacctc ccgacctaca cccttgaggc tgtatacgag | 840 |
| gcggttttctg gcaagcccaa ggagaaggtc tacgccgagg agatagccac cgcctgggag | 900 |
| accggcgagg ggcttgagag ggtcgcgcgc tactcgatgg aggacgcgag ggttacctac | 960 |
| gagcttggca gggagttctt cccgatggag gccagcttt ccaggctcat cggccaaggc | 1020 |
| ctctgggacg tttcccgctc cagcaccggc aacctcgtcg agtggttcct cctaaggaag | 1080 |
| gcctacgaga ggaacgaact cgctcccaac aagcccgacg agagggagct ggcgaggaga | 1140 |
| agggggggct acgccggtgg ctacgtcaag gagccggagc ggggactgtg ggacaatatc | 1200 |
| gtgtatctag actttcgtag tctctaccct tcaatcataa tcaccacaa cgtctcgcca | 1260 |
| gatacgctca accgcgaggg gtgtaggagc tacgacgttg ccccgagggt cggtcacaag | 1320 |
| ttctgcaagg acttccccgg cttcattccg agcctgctcg gaaacctgct ggaggaaagg | 1380 |
| cagaagataa agaggaagat gaaggcaact ctcgaccgcg tggagaagaa tctcctcgat | 1440 |
| tacaggcaac gcgccatcaa gattctcgcc aacagctact acggctacta cggctatgcc | 1500 |
| agggcaagat ggtactgcag ggagtgcgcc gagagcgtaa cggcatgggg aaggaggtac | 1560 |

| | | | | | | |
|------------|-------------|------------|------------|-------------|------------|----------------------|
| atcgaaatgg | tcatcagaga | gcttgaggaa | aagttcggtt | ttaaagtcct | ctatgcagac | 1620 |
| acagacggtc | tccatgccac | cattcctgga | gcggacgctg | aaacagtcaa | gaaaaaggca | 1680 |
| atggagttct | taaactatat | caatcccaaa | ctgcccggcc | ttctcgaaact | cgaatacgag | 1740 |
| ggcttctacg | tcagggggctt | cttcgtcacg | aagaaaaagt | acgcggtcat | cgacgaggag | 1800 |
| ggcaagataa | ccacgcgcgg | gcttgagata | gtcaggcgcg | actggagcga | gatagcgaag | 1860 |
| gagacgcagg | cgaggggttt | ggaggcgata | ctcaggcacg | gtgacgttga | agaggccgtc | 1920 |
| agaattgtca | gggaagtcac | cgaaaagctg | agcaagtacg | aggttccgcc | ggagaagctg | 1980 |
| gttatccacg | agcagataac | gcgcgagctc | aaggactaca | aggccaccgg | cccgcacgta | 2040 |
| gccatagcga | agcgtttggc | cgccagaggt | gttaaaatcc | ggcccggaac | tgtgataagc | 2100 |
| tacatcgttc | tgaagggctc | cggaaggata | ggcgacaggg | cgattccctt | cgacgagttc | 2160 |
| gacccgacga | agcacaagta | cgatgcggac | tactacatcg | agaaccaggt | tctgccggca | 2220 |
| gttgagagaa | tcctcagggc | cttcggctac | cgcaaggaag | acctgcgcta | ccagaagacg | 2280 |
| aggcaggteg | ggcttggcgc | gtggctgaag | ccgaagggga | agaagaagtg | a | 2331 (SEQ ID NO: 11) |